

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 16, 2004, 11:08:12 ; Search time 49 seconds
(without alignments)
1586.865 Million cell updates/sec

Title: US-10-018-672-2
Perfect score: 1383
Sequence: 1 MNEFKINGICALASGIALAG.....TDEVEAEAKQKQDGVKGVKGV 276

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1158786 seqs, 281726120 residues

Total number of hits satisfying chosen parameters: 1158786

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pap.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pap.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pap.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pap.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pap.*
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- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pap.*
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- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pap.*
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- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pap.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pap.*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pap.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1368	98.9	276	12 US-10-282-122A-63386	Sequence 63386, A
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3	1007.5	72.8	273	12 US-10-380-817-4	Sequence 4, Appli
4	1007.5	72.8	273	12 US-10-380-817-8	Sequence 8, Appli
5	1007.5	72.8	273	12 US-10-380-817-10	Sequence 10, Appli
6	1006.5	72.8	273	9 US-09-815-242-11067	Sequence 11067, A
7	1006.5	72.8	273	12 US-10-282-122A-58240	Sequence 58240, A
8	1006.5	72.8	273	12 US-10-380-817-6	Sequence 6, Appli
9	888	64.2	276	12 US-10-282-122A-67387	Sequence 67387, A
10	793.5	57.4	271	12 US-10-282-122A-76195	Sequence 76195, A
11	782.5	56.6	271	9 US-09-815-242-10050	Sequence 10050, A
12	782.5	56.6	271	12 US-10-282-122A-43291	Sequence 43291, A
13	780.5	56.4	271	12 US-10-282-122A-55826	Sequence 55826, A
14	775.5	56.1	271	12 US-10-282-122A-59600	Sequence 59600, A
15	757.5	54.8	271	12 US-10-282-122A-68391	Sequence 68391, A

16	757.5	54.8	271	12 US-10-282-122A-78174	Sequence 78174, A
17	751.5	54.3	275	12 US-10-282-122A-77174	Sequence 77174, A
18	743.5	53.8	240	9 US-09-815-242-11656	Sequence 11656, A
19	562	40.6	295	12 US-10-282-122A-47704	Sequence 47704, A
20	551	39.8	262	12 US-10-282-122A-51371	Sequence 51371, A
21	549.5	39.7	272	12 US-10-282-122A-50375	Sequence 50375, A
22	545	39.4	256	12 US-10-282-122A-61127	Sequence 61127, A
23	540	39.0	268	12 US-10-282-122A-49256	Sequence 49256, A
24	527.5	38.1	270	12 US-10-282-122A-49339	Sequence 49339, A
25	526.5	38.1	265	12 US-10-282-122A-51201	Sequence 51201, A
26	506.5	36.6	261	12 US-10-282-122A-67692	Sequence 67692, A
27	502.5	36.3	260	9 US-09-815-242-12110	Sequence 12110, A
28	502.5	36.3	260	12 US-10-282-122A-66844	Sequence 66844, A
29	497.5	36.0	259	9 US-09-815-242-5146	Sequence 5146, Ap
30	494	35.7	263	12 US-10-282-122A-43469	Sequence 43469, A
31	488	35.3	256	12 US-10-282-122A-52376	Sequence 52376, A
32	487	35.2	257	12 US-10-282-122A-67627	Sequence 67627, A
33	481	34.8	277	12 US-10-282-122A-69359	Sequence 69359, A
34	481	34.8	277	12 US-10-282-122A-57209	Sequence 57209, A
35	477.5	34.5	257	12 US-10-282-122A-54418	Sequence 54418, A
36	472.5	34.2	270	12 US-10-282-122A-52496	Sequence 52496, A
37	472.5	34.1	270	12 US-10-282-122A-52838	Sequence 52838, A
38	468	33.8	256	12 US-10-282-122A-54417	Sequence 54417, A
39	467.5	33.8	271	9 US-09-815-242-11460	Sequence 11460, A
40	467.5	33.8	271	12 US-10-282-122A-59034	Sequence 59034, A
41	462.5	33.4	271	9 US-09-815-242-11624	Sequence 11624, A
42	462.5	33.4	271	12 US-10-335-977-4882	Sequence 4882, Ap
43	462.5	33.4	271	12 US-10-335-977-4883	Sequence 4883, Ap
44	462.5	33.4	273	12 US-10-282-122A-60558	Sequence 60558, A
45	462.5	33.4	273	12 US-10-282-122A-60558	Sequence 60558, A

check pricing for New 102(e) Jul 05/05 101

RESULT 1

US-10-282-122A-63386

Sequence 63386, Application US/10282122A

Publication No: US20040029129A1

GENERAL INFORMATION:

APPLICANT: Wang, Liangsu

APPLICANT: Zamudio, Carlos

APPLICANT: Malone, Cheryl

APPLICANT: Haselbeck, Robert

APPLICANT: Ohlsen, Kari

APPLICANT: Zyskind, Judith

APPLICANT: Wall, Daniel

APPLICANT: Trawick, John

APPLICANT: Carr, Grant

APPLICANT: Yamamoto, Robert

APPLICANT: Forsyth, R.

APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

FILE REFERENCE: ELITRA.034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR FILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR FILING DATE: 2000-09-09

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/267,636

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OM protein - protein search, using sw model

Run on: June 16, 2004, 11:00:51 ; Search time 18 Seconds
(without alignments)
798.409 Million cell updates/sec

Title: US-10-018-672-2

Perfect score: 1383

Sequence: 1 MNFGKINGICALASGIALAG.....TDEVEAAKKQKDGVIKGM 276

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1012.5	73.2	277	1 PLPA_PASHA	Q08688 pasteurella
2	1006.5	72.8	273	1 METO_HAEN	R31728 haemophilus
3	888	64.2	276	1 METO_PASMU	Q9ck95 pasteurella
4	793.5	57.4	271	1 METO_SALTI	Q82992 salmonella
5	792.5	57.3	271	1 METO_SALTY	Q82991 salmonella
6	791.5	57.2	263	1 PLPC_PASHA	Q08870 pasteurella
7	791.5	57.2	271	1 METO_ECO57	Q8x8v5 escherichia
8	782.5	56.6	271	1 METO_ECOLI	P28635 escherichia
9	773	55.9	276	1 PLPB_PASHA	Q08869 pasteurella
10	757.5	54.8	271	1 METO_YERPE	Q8240 versinia pe
11	751.5	54.3	269	1 METO_VIRCH	Q9ktj7 vibrio chol
12	691.5	50.0	272	1 NLPA_ECOLI	P04846 escherichia
13	686.5	49.6	272	1 NLPA_ECO57	Q0xc50 escherichia
14	416.5	30.1	268	1 TP32_TREPA	Q07950 treponema p
15	296	21.4	263	1 YHCJ_BACSU	P54594 bacillus su
16	112.5	8.1	2867	1 RBP2_PLAVD	Q00799 plasmodium
17	106	7.7	1592	1 GTF2_STRDO	P27470 streptococ
18	104.5	7.6	991	1 SCMA_RICAU	Q2aj64 rickettsia
19	103.5	7.5	543	1 CH60_MYGE	P47632 mycoplasma
20	103	7.4	1597	1 GTF1_STRDO	P11001 streptococ
21	99.5	7.2	465	1 APEA_CLOAB	Q97k30 clostridium
22	99	7.2	814	1 SLAI_BACAA	P49051 bacillus an
23	99	7.2	928	1 HXAZ_HAEN	P45354 haemophilus
24	98.5	7.1	459	1 TMEE_CLOTE	Q89942 clostridium
25	98	7.1	469	1 Y889_MERJA	Q58299 methanococ
26	97.5	7.0	306	1 OFBC_BACSU	Q45462 bacillus su
27	97.5	7.0	1164	1 BAG_STRAG	P27951 streptococ
28	97	7.0	1036	1 Y414_MYGE	P47653 mycoplasma
29	96.5	7.0	339	1 PUR5_OCEIH	Q8es94 oceanobacil
30	96.5	7.0	2144	1 GLT1_YEAST	Q12680 saccharomy
31	96	6.9	382	1 VATC_HUMAN	P21283 homo sapien
32	96	6.9	428	1 AROA_CAMJE	P52332 campylobact
33	96	6.9	525	1 SPI_PARFA	Q05308 rareobacter

ALIGNMENTS

RESULT 1

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AC	Q08868; Q07363;			
DT	01-NOV-1995 (Rel. 32, Created)			
DT	01-NOV-1995 (Rel. 32, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Outer membrane lipoprotein 1 precursor (PLP1).			
GN	PLPA.			
OS	Pasteurella haemolytica.			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;			
OC	Pasteurellaceae; Mannheimia.			
OX	NCBI_TaxID=75985;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=serotype A1;			
RC	MEDLINE=93328110; PubMed=8335249;			
RA	Murphy G.L., Whitworth L.C.;			
RT	"Analysis of tandem, multiple genes encoding 30-kDa membrane proteins			
RT	in Pasteurella haemolytica A1.;"			
RL	Gene 129:107-111(1993).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=serotype A1;			
RC	MEDLINE=94011378; PubMed=8406866;			
RA	Cooney B.J., Lo R.Y.C.;			
RT	"Three contiguous lipoprotein genes in Pasteurella haemolytica A1			
RT	which are homologous to a lipoprotein gene in Haemophilus influenzae			
RT	type b.;"			
RL	Infect. Immun. 61:4682-4688(1993).			
CC	-!- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid			
CC	anchor (Probable).			
CC	-!- SIMILARITY: Belongs to the nlpa lipoprotein family.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation.			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
CC	EMBL; L11037; AAA2538.1; -			
CC	EMBL; M91072; AAA25541.1; -			
CC	EMBL; L16627; AAA25546.1; -			
CC	PIR; JN0751; JN0751.			
CC	InterPro; IPR004872; Lipoprotein_9.			
CC	InterPro; IPR000437; Prok_lipoprot_9.			
CC	PIfam; PF03180; Lipoprotein_9; 1.			
CC	TIGRFAMs; TIGR00363; TIGR00363; 1.			
CC	PROSITE; PS0013; PROKAR LIPOPROTEIN; 1.			
CC	Outer membrane; Lipoprotein; Signal; Multigene family; Palmitate.			
CC	POTENTIAL.			
CC	OUTER MEMBRANE LIPOPROTEIN 1.			
CC	CHAIN 1 19			
CC	20 277			
CC	20 20			
CC	N-palmitoyl cysteine (Probable).			

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OM protein - protein search, using sw model

Run on: June 16, 2004, 11:05:36 ; Search time 22 Seconds
(without alignments)
647.671 Million cell updates/sec

Title: US-10-018-672-2
Perfect score: 1383
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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5: /cgn2_6/ptodata/2/iaa/PTCUS-COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles!.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	775.5	56.1	289	4	US-09-489-039A-12337
2	757.5	54.8	279	4	US-09-543-681A-6534
3	685.5	49.6	285	4	US-09-489-039A-10641
4	671.5	48.6	279	4	US-09-543-681A-4548
5	651.5	47.1	272	4	US-09-489-039A-10410
6	596	43.1	279	4	US-09-543-681A-6914
7	520	37.6	118	4	US-09-540-236-2991
8	503.5	36.4	306	4	US-09-252-991A-18873
9	494.5	35.8	271	4	US-09-252-991A-20200
10	481	34.8	277	4	US-09-071-035-30
11	481	34.8	278	4	US-09-134-000C-4965
12	475	34.3	269	4	US-09-543-681A-4774
13	462	33.4	257	4	US-09-071-035-32
14	449.5	32.5	291	4	US-09-107-532A-7234
15	441	31.9	288	4	US-09-134-001C-4005
16	416	30.1	280	4	US-08-956-171E-5195
17	373.5	27.0	279	4	US-09-134-001C-4878
18	366	26.5	269	4	US-09-107-532A-6443
19	364	26.3	296	4	US-09-328-352-6924
20	364	26.3	326	4	US-09-489-039A-9512
21	358.5	25.9	261	4	US-09-634-238-420
22	356	25.7	260	3	US-08-961-083-32
23	356	25.7	260	4	US-09-536-784-32
24	346	25.0	273	4	US-08-956-171E-5196
25	337.5	24.4	286	4	US-09-328-352-6702
26	335	24.2	304	4	US-09-328-352-7028
27	325.5	23.5	294	4	US-09-328-352-5549

28	324	23.4	272	4	US-09-071-035-22	Sequence 22, Appl
29	322	23.3	342	4	US-09-252-991A-25420	Sequence 25420, A
30	321.5	23.2	280	4	US-09-489-039A-13968	Sequence 13968, A
31	319.5	23.1	220	4	US-09-634-238-283	Sequence 283, App
32	318	23.0	251	4	US-09-071-035-24	Sequence 24, Appl
33	315.5	22.8	272	4	US-09-071-035-10	Sequence 10, Appl
34	308.5	22.3	253	4	US-09-071-035-12	Sequence 12, Appl
35	304.5	21.8	278	4	US-09-134-000C-5006	Sequence 5006, Ap
36	257.5	18.6	275	4	US-09-198-452A-291	Sequence 291, App
37	209	15.1	306	4	US-09-489-039A-10023	Sequence 10023, A
38	108	7.8	91	4	US-09-134-000C-3687	Sequence 3687, Ap
39	106	7.7	347	4	US-09-328-352-6764	Sequence 6764, Ap
40	105	7.6	794	4	US-09-134-000C-5518	Sequence 5518, Ap
41	103	7.4	503	4	US-09-071-035-360	Sequence 360, App
42	103	7.4	1074	4	US-09-071-035-358	Sequence 358, App
43	103	7.4	1074	4	US-09-071-035-394	Sequence 394, App
44	103	7.4	1096	4	US-09-071-035-5764	Sequence 5764, Ap
45	102.5	7.4	308	4	US-09-134-000C-4400	Sequence 4400, Ap

ALIGNMENTS

RESULT 1
US-09-489-039A-12337
; Sequence 12337, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 12337
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12337

Query Match	56.1%;	Score	775.5;	DB 4;	Length	289;			
Best Local Similarity	55.2%;	Pred.No.	3.3e-73;						
Matches	153;	Conservative	45;	Mismatches	68;	Indels 11; Gaps 3;			
QY	2	NFGKINGICALASG	TALAGCSNQSN	EPAAISKTAAQT	KVGMAGPQ	QAVAEVAGQVAK	61		
DB	22	NFKTFAAVGALIT	GSIALVCGQDEK	P-----	NH	KVGVIVGAEQ	QVAVAKVAK	73	
QY	62	KYNLTVELVEFND	YAMPNSAVSK	GELDANAMQHP	EKDPKLEK	SOEKLNNLV	IGNTFVYPL	121	
DB	74	KGLDVELVTFND	YVLPNEALS	SGDIDVNAFQ	HKPYLDQQIK	DGRY-KLVA	IGNTFVYPI	132	
QY	122	AGYSTKIKTLNEL	KDGIATVDP	SPNLSARALIL	EKGLIK	KDKNTNLF	FSITLIDVNP	181	
DB	133	AGYSKKIKSLDEL	QPSQIAVP	NDPTNLGRSL	LLIQVGLIK	KDKGVGLL	PTSLDVENP	192	
QY	182	KGLVIKEVDTS	AAAIID--	VDLAVANN	YAGOVGLT	ASENGVE	VEDKDS	SPYNNIIVAR	239
DB	193	KNLKVELEAPOL	PSLDDAQIA	LAVINTTASQ	IGLTPAKD	IGFVEK	ESPYNNLIVAR	252	
QY	240	ADNKSKAIQDF	VKAYQITDE	VEAEAKQF	KDGVKGM	276			
DB	253	EDNKAENVKVF	QAYQSD	DEVVEAEANK	IFNGGAVKGM	289			

RESULT 2
US-09-543-681A-6534
; Sequence 6534, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:

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OM protein - protein search, using sw model

Run on: June 16, 2004, 11:04:11 ; Search time 46 Seconds
(without alignments)

Title: US-10-018-672-2
 Perfect score: 1383
 Sequence: 1 MNFGKINGICALASGIALAG.....TDEVEAKKQFKDGVTKGW 276

Scoring table: BLOSUM62

Searched: 1017041 segs. 315518202

Total number of hits satisfying chosen parameter

Minimum DB seq length: 0

[illegible]

Maximum Match 100

SECRET

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1: sp_archea:
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1: sp:amphibia.*
2: sp:amphibia.*
3: sp:fungi.*
4: sp:human.*
5: sp:invertebrate.*
6: sp:mammal.*
7: sp:mhc.*
8: sp:organelle.*
9: sp:phase.*
10: sp:plant.*
11: sp:rodent.*
12: sp:virus.*
13: sp:veterate.*
14: sp:unclassified.*
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16: sp:backetiarp.*
17: sp:archaea.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	958.5	69.3	270	16	Q7VM93	haemophilus
2	786.5	56.9	271	16	Q83MC6	shigella fl
3	770	55.7	270	16	Q8CWC8	escherichia
4	752.5	54.4	269	16	Q8DFC1	vibrio vuln
5	739.5	53.5	269	16	Q87RS3	vibrio para
6	685.5	49.6	272	16	Q8CVK2	escherichia
7	571.5	41.3	267	16	Q83F42	coxiella bu
8	571	41.3	259	2	Q69441	legionella
9	563.5	40.7	266	16	Q8Y0X1	raistonia s
10	560.5	40.5	278	16	Q8YD39	brucella me
11	560.5	40.5	278	16	Q8FY86	brucella su
12	554	40.1	262	16	Q7W3J7	bordetella
13	553	40.0	262	16	Q7WSW2	bordetella
14	551	39.8	262	16	Q7WSM1	bordetella
15	527.5	38.1	265	16	Q7WFF1	bordetella
16	527.5	38.1	265	16	Q7W4E3	bordetella

17	526.5	38.1	265	16	Q7VV70	Q7vv70	bordetella
18	524.5	37.9	358	16	Q92LX5	Q92lx5	rhizobium m
19	517.5	37.4	529	16	Q8XU08	Q8xu08	ralstonia s
20	517.0	37.4	261	16	Q8RFN4	Q8rfn4	fusobacteri
21	517	37.4	284	16	Q88DA1	Q88da1	rhizobium 1
22	515.5	37.3	359	16	Q8U7G0	Q8u7g0	agrobacteri
23	513	37.1	307	16	Q89E28	Q89e28	bradyrhizob
24	509.5	36.8	286	16	Q9CIN7	Q9cin7	lactococcus
25	507	36.7	259	16	Q8PFX4	Q8pfx4	brucella su
26	507	36.7	268	16	Q8YEC4	Q8yec4	brucella me
27	506.5	36.6	261	16	Q88CL5	Q88cl5	pseudomonas
28	502.5	36.3	260	16	Q8HT68	Q8ht68	pseudomonas
29	501	36.2	259	16	Q8PGF0	Q8pgf0	xanthomonas
30	497.5	36.0	259	16	Q8XH85	Q8xh85	pseudomonas
31	497.5	36.0	266	16	Q8P4S9	Q8p4s9	xanthomonas
32	488	35.3	256	16	Q88RL7	Q88rl7	pseudomonas
33	487	35.2	257	16	Q87UN6	Q87un6	pseudomonas
34	485	35.1	268	16	Q7VI95	Q7vi95	helicobacte
35	481	34.8	277	16	Q83ZY8	Q83zy8	enterococcu
36	477.5	34.5	257	16	Q9PPE7	Q9ppe7	campylobact
37	469.5	33.9	273	16	Q8ELA4	Q8ela4	oceanobacil
38	468	33.8	256	16	Q9PPE8	Q9ppe8	campylobact
39	467.5	33.8	271	16	Q26084	Q26084	helicobacte
40	464.5	33.6	286	16	Q9CIN6	Q9cin6	lactococcus
41	463.5	33.5	273	16	Q2E2E5	Q2e2e5	listeria in
42	462.5	33.4	271	16	Q92J45	Q92j45	helicobacte
43	462.5	33.4	273	16	Q8YA74	Q8ya74	listeria mo
44	460	33.3	286	16	Q9CIN8	Q9cin8	lactococcus
45	457.5	33.1	260	16	Q97UT0	Q97ut0	pseudomonas

ALIGNMENTS

RESULT 1

Q7VM93	PRELIMINARY; PRT; 270 AA.
ID	Q7VM93
AC	Q7VM93;
DT	01-OCT-2003 (T-EMBLrel. 25, Created)
DT	01-OCT-2003 (T-EMBLrel. 25, Last sequence update)
DT	01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE	28Kda outer membrane lipoprotein.
GN	HLPA OR HD1100.
OS	Haemophilus ducreyi.
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC	Pasteurellaceae; Haemophilus.
OX	NCBI_TaxID=730;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=3500HP / ATCC 700724;
RA	Munson R.S. Jr., Ray W.C., Mahairas G., Sabo P., Mungur R.,
RA	Johnson L., Nguyen D., Wang J., Forst C., Hood L.;
RT	"The complete genome sequence of Haemophilus ducreyi.";
RL	Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
RR	EMBL; AS017153; AAP95966.1; -
RD	Lipoprotein; Complete proteome.
SK	SEQUENCE 270 AA; 29535 MW FC077F10B13304AD CRC64;

	Query Match	69.3%	Score 958.5	DB 16	Length 270
	Best Local Similarity	71.5%	Pred. No. 1.4e-53		
	Matches 188	Conservative 34	Mismatches 36	Indels 5	Gaps 2
QY	14	SGIALGCSNQSNPEAPRAISKTAQTIKVCVMAGPQCAVEAGQVAKKYNLTVELVEFN	73		
Db	13	STLALTCKCPANNQ----GDSASTKIKGVMSGPEHSAEAKAEIAKQKNLEYEFVLFN	68		
QY	74	DYAMPNSAVSKGBILDANAMQHPKPYLEKDSQKGLNNLVIGNTFFVYPLAGYSTKIKTLE	133		
Db	69	DYALPNMAVSKGLDIDNANMQHPFYLDKDSQKGLNNLVIVGNAFVYPLAGYSKKIKNAE	128		
QY	134	LKOGATVAPNDPSNARALILLEKQGLIKLKONTNLFSTTLDIVENPKKLVITKEVDTSV	193		
Db	129	LKSAVAVAPNDPSNARALMLEKQGLTNDNTNINFAFKLDIVDPKKLIIKEVDTSV	188		

GenCore version 5.1.6
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OM protein/- protein search, using sw model

Run on: June 16, 2004, 11:00:16 ; Search time 60 Seconds
(without alignments)
1299.719 Million cell updates/sec

Title: US-10-018-672-2

Perfect score: 1383

Sequence: 1 MNFKINGICALASGIALAG.....TDEVEAEAKQKQGVKIGW 276

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04.*

1: Geneseq1980s.*

2: Geneseq1990s.*

3: Geneseq2000s.*

4: Geneseq2001s.*

5: Geneseq2002s.*

6: Geneseq2003as.*

7: Geneseq2003bs.*

8: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1383	100.0	276	4	AAB20104 Moraxella
2	1368	98.9	276	5	AAO17582 M catarrh
3	1368	98.9	276	6	ABU35462 Protein e
4	1007.5	72.8	273	5	ABU35462 Protein e
5	1006.5	72.8	273	4	AAU35474 Haemophil
6	1006.5	72.8	273	5	ABU35474 Haemophil
7	1006.5	72.8	273	6	ABU30316 Protein e
8	1004	72.6	272	5	AAO17813 H influen
9	888	64.2	276	6	ABU39463 Protein e
10	793.5	57.4	271	6	ABU48271 Protein e
11	782.5	56.6	271	4	AAU34457 E. coli c
12	782.5	56.6	271	6	ABU15367 Protein e
13	780.5	56.4	271	6	ABU27902 Protein e
14	775.5	56.1	271	6	ABU31676 Protein e
15	767.5	55.5	272	6	ABU67576 Photorhab
16	757.5	54.8	271	6	ABU50250 Protein e
17	757.5	54.8	271	6	ABU40467 Protein e
18	751.5	54.3	275	6	ABU49250 Protein e
19	743.5	53.8	240	4	AAU36063 Klebsiell
20	562	40.6	295	6	ABU19780 Protein e
21	551	39.8	262	6	ABU23447 Protein e
22	549.5	39.7	272	6	ABU22451 Protein e
23	545	39.4	256	6	ABU33203 Protein e
24	540	38.0	268	6	ABU21332 Protein e
25	527.5	38.1	270	6	ABU21415 Protein e

N/C
-N6 mm

RESULT 1

AAB20104

ID AAB20104 standard; protein; 276 AA.

XX AAB20104;

XX AC AAB20104;

XX DT 23-APR-2001 (first entry)

XX DE Moraxella catarrhalis BASB111 protein.

XX DE DE Moraxella catarrhalis BASB111 protein.

XX DE DE Moraxella catarrhalis BASB111 protein.

XX DE DE Moraxella catarrhalis BASB111 protein.

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ALIGNMENTS

Abu23277 Protein e
Abu33625 Lactococ
Abu39768 Protein e
Abu36517 Pseudom
Abu38920 Protein e
Abu33650 Pseudom
Abu15545 Protein e
Abu29703 Protein e
Abu39703 Protein e
Abu41435 Protein e
Aay00024 Enterococ
ABP43243 E faecal
Abu88271 E. faecal
Abu29285 Protein e
Abu13522 Enterococ
Abu26494 Protein e
Abu24572 Protein e
Abu24914 Protein e
Abu26493 Protein e
AAW90023 Expressed

26 526.5 38.1 265 6 ABU23277
27 509.5 36.8 286 5 ABU33625
28 506.5 36.6 261 6 ABU39768
29 502.5 36.3 260 4 AAU36517
30 502.5 36.3 260 6 ABU38920
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33 494 35.7 263 6 ABU29703
34 488 35.3 256 6 ABU39703
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42 472.5 34.2 270 6 ABU24572
43 472 34.1 270 6 ABU24914
44 468 33.8 256 6 ABU26493
45 467.5 33.8 271 2 AAW90023

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